Output files from different CRISPR-Cas detection tools

CASC

- **results.txt** summary

```
#seq_id array_id        spacers array_start     array_stop      mean_spacer_len stddev_spacer_len       bonafide        code
1       1       18      2293915 2295042 32.056  0.236   true    7
1       2       28      2304214 2305952 32.071  0.262   true    7
```

Coding scheme (last column):

Code	(Binary)	Cas Protein Hit	Matches Known Repeat	Proper Statistics
0	000	no	no	no
1	001	no	no	Yes
2	010	no	Yes	no
3	011	no	Yes	Yes
4	100	Yes	no	no
5	101	Yes	no	Yes
6	110	Yes	Yes	no
7	111	Yes	Yes	Yes

- **bonafide.repeats.fasta**
  bonafide.spacers.fasta
  non-bonafide.repeats.fasta
  non-bonafide.spacers.fasta

```
>1-repeat-1-1
GTGTTCCCCACGGGTGTGGGGATGAACCA
>1-repeat-1-2
GTGTTCCCCACGGGTGTGGGGATGAACCG
>1-repeat-1-3
GTGTTCCCCACGGGTGTGGGGATGAACCG
>1-repeat-1-4
GTGTTCCCCACGGGTGTGGGGATGAACCG
>1-repeat-1-5
GTGTTCCCCACGGGTGTGGGGATGAACCG
>1-repeat-1-6
GTGTTCCCCACGGGTGTGGGGATGAACCG
```

```
>1-spacer-1-1
GCAGGATTTGGAGTCGGAGCGTTTACCTACAT
>1-spacer-1-2
GTGAACGATGCGAATCGGGCGGGGGTTTGGTC
>1-spacer-1-3
GCTTGGTAGATGCCTGGAACAAGTCGGTCAGC
>1-spacer-1-4
CGCGCTGTCCTCGGCCTGGACTGGACCATCGA
>1-spacer-1-5
TGGGCGAACGACGGCAGCGTCACCCAGGCGCA
>1-spacer-1-6
ACAGGGACGTTCTCCGCGAGCTGGCCATCGAC
```

- **report.md**

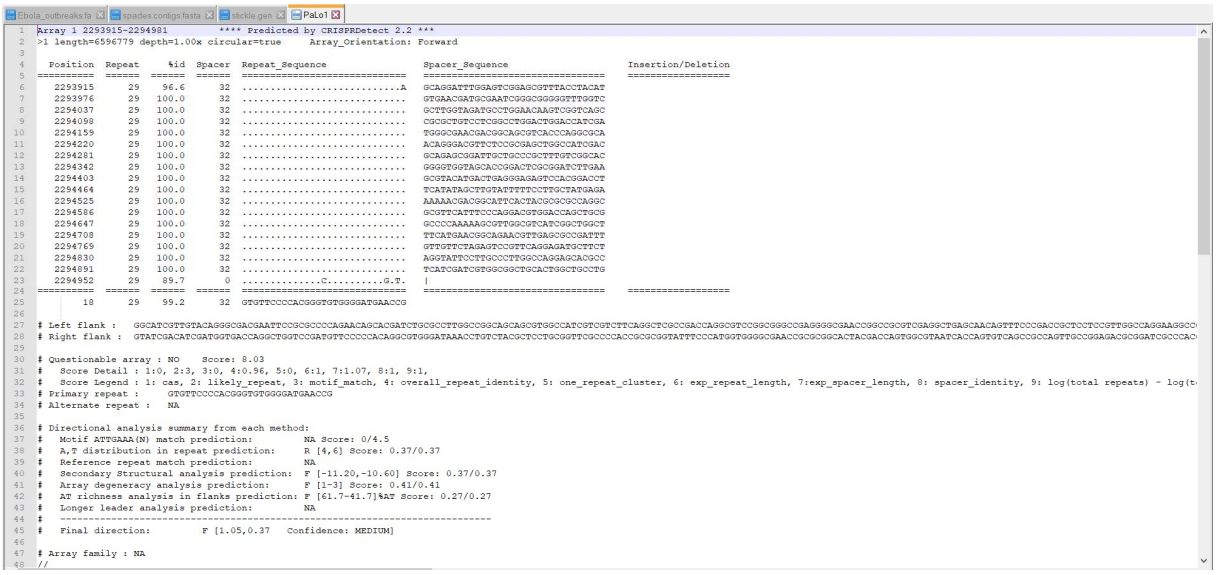
```
CASC Report
===========

### Input Summary

- Input File: /mnt/blastdb/emma/crispr_annotation/assembly/unicycler/PaLo1/assembly.fasta
- Number of Sequences = 2
- Number of Bases = 6600643
- Bases per Sequence = 3300322
- Mode = Liberal

### CRISPR Identification
- Putative CRISPR arrays found = 1
- Bona fide CRISPR arrays = 2 (200%)
- Arrays with Cas protein upstream = 1
- Arrays with repeats matching known CRISPR repeats = 1
- Arrays with proper statistics (liberal mode only) = 2
```

- **casc.log**

```
Commandline: ./casc -i /mnt/blastdb/emma/crispr_annotation/assembly/unicycler/PaLo1/assembly.fasta -o /mnt/

Output Directory: /mnt/blastdb/emma/crispr_tools/Try/CASC/PaLo1
Mode: Liberal

===== CASC Started. Log can be found here: /mnt/blastdb/emma/crispr_tools/Try/CASC/PaLo1/casc.log

== Spliting the FASTA file ........................... Done [22Oct2019 15:30]
== Running mCRT to find putative spacers ............. Done [22Oct2019 15:30]
== Extracting sequences with putative spacers ........ Done [22Oct2019 15:30]
== Comparing putative repeats against the repeat DB ... Done [22Oct2019 15:30]
== Searching for Cas proteins ........................ Done [22Oct2019 15:57]
== Gathering and printing results .................... Done [22Oct2019 15:57]

===== CASC Finished!

CASC log can be found here: /mnt/blastdb/emma/crispr_tools/Try/CASC/PaLo1/casc.log
```

CRISPRDetect

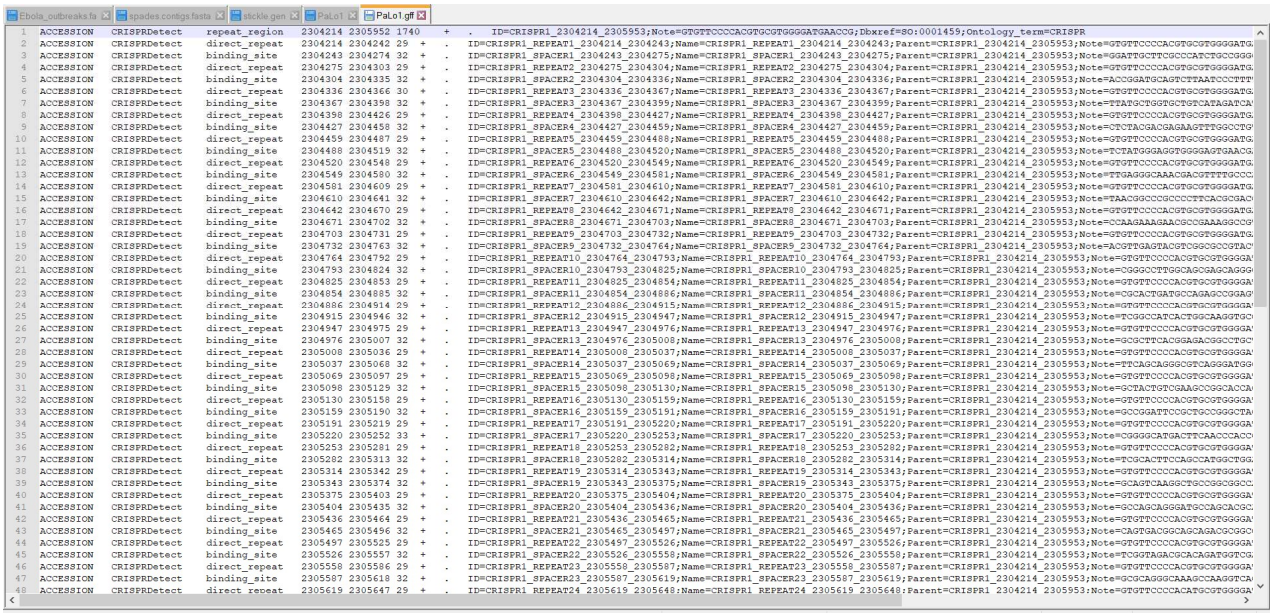
- **.txt** summary



```
Array 1 2293915-2294981          **** Predicted by CRISPRDetect 2.2 ***
>1 length=6596779 depth=1.00x circular=true     Array_Orientation: Forward

  Position  Repeat     %id  Spacer  Repeat_Sequence                 Spacer_Sequence                 Insertion/Deletion
  ========  ======  ======  ======  ==============================  ==============================  ==================
   2293915      29    96.6      32  ..............................A  GCAGGATTTGGAGTCGGAGCGTTTACCTACAT
   2293976      29   100.0      32  ..............................  GTGAACGATGCGAATCGGGCGGGGGGTTTGGTC
   2294037      29   100.0      32  ..............................  GCTTGGTAGATGCCTGGAACAAGTCGGTCAGC
   2294098      29   100.0      32  ..............................  CGCGCTGTCCTCGGCCTGGACTGGACCATCGA
   2294159      29   100.0      32  ..............................  TGGGCGAACGACGGCAGCGTCACCCAGGCGCA
   2294220      29   100.0      32  ..............................  ACAGGGACGTTCTCCGCGAGCTGGCCATCGAC
   2294281      29   100.0      32  ..............................  GCAGACGCGATTGCTGCCCGCTTTGTCGGCAC
   2294342      29   100.0      32  ..............................  GGGGTGGTAGCACCGGACTCGCGGATCTTGAA
   2294403      29   100.0      32  ..............................  GCGTACATGACTGAGGGAGAGTCCACGGACCT
   2294464      29   100.0      32  ..............................  TCATATAGCTTGTATTTTTCCTTGCTATGAGA
   2294525      29   100.0      32  ..............................  AAAAACGACGGCATTCACTACGCGCGCCAGGC
   2294586      29   100.0      32  ..............................  GCGTTCATTTCCCAGGACGTGGACCAGCTGCG
   2294647      29   100.0      32  ..............................  GCCCCAAAAAGCGTTGGCGTCATCGGCTGGCT
   2294708      29   100.0      32  ..............................  TTCATGAACGGCAGAACGTTGAGCGCGATTT
   2294769      29   100.0      32  ..............................  GTTGTTCTAGAGTCCGTTCAGGAGATGCTTCT
   2294830      29   100.0      32  ..............................  AGGTATTCCTTGCCCTTGGCCAGGAGCACGCC
   2294891      29   100.0      32  ..............................  TCATCGATCGTGGCGGCTGCACTGGCTGCCTG
   2294952      29    89.7       0  ..............C..........G.T.  |
==========  ======  ======  ======  ==============================  ==============================  ==================
         18      29    99.2      32  GTGTTCCCCACGGGTGTGGGGATGAACCG

# Left flank :   GGCATCGTTGTACAGGGCGACGAATTCCGCGCCCCAGAACAGCACGATCTGCGGCCTTGGCCGGCAGCAGCGTGGCCATCGTCGTCTTCAGGCTCGCCGACCAGGCGTCCGGCGGGCCGAGGGGCGAACCGGCCGCGTCGAGGCTGAGCAACAGTTCCCGACCGCTCCTCCGTTGGCCAGGAAGGCC
# Right flank :  GTATCGACATCGATGGTGACCAGGCTGGTCCGATGTTCCCCCACAGGCGTGGGATAAACCTGTCTACGCTCCTGCGGTTCGCCCCACCGCGCGGTATTTCCCATGGTGGGGCGAACCGCGCGGCACTACGACCAGTGGCGTAATCACCAGTGTCAGCCGCCAGTTGCCGGAGACGCGGATCGCCCAC

# Questionable array : NO    Score: 8.03
#   Score Detail : 1:0, 2:3, 3:0, 4:0.96, 5:0, 6:1, 7:1.07, 8:1, 9:1,
#   Score Legend : 1: cas, 2: likely_repeat, 3: motif_match, 4: overall_repeat_identity, 5: one_repeat_cluster, 6: exp_repeat_length, 7:exp_spacer_length, 8: spacer_identity, 9: log(total repeats) - log(t
# Primary repeat :    GTGTTCCCCACGGGTGTGGGGATGAACCG
# Alternate repeat :  NA

# Directional analysis summary from each method:
#   Motif ATTGAAA(N) match prediction:        NA Score: 0/4.5
#   A,T distribution in repeat prediction:    R [4,6] Score: 0.37/0.37
#   Reference repeat match prediction:        NA
#   Secondary Structural analysis prediction: F [-11.20,-10.60] Score: 0.37/0.37
#   Array degeneracy analysis prediction:     F [1-3] Score: 0.41/0.41
#   AT richness analysis in flanks prediction: F [61.7-41.7]%AT Score: 0.27/0.27
#   Longer leader analysis prediction:        NA
#   ----------------------------------------------------------------
#   Final direction:          F [1.05,0.37   Confidence: MEDIUM]

# Array family : NA
//
```

(but normally CAS data should be there: did not work even though a gbk file was supplied)

- **.fp** filtered repeats (didn't meet the minimum evidence level): mostly empty
- .**gff** annotation → visualization in CRISPRStudio



```
ACCESSION  CRISPRDetect  repeat_region  2304214 2305952 1740  +  .  ID=CRISPR1_2304214_2305953;Note=GTGTTCCCCACGTGCGTGGGGATGAACCG;Dbxref=SO:0001459;Ontology_term=CRISPR
ACCESSION  CRISPRDetect  direct_repeat  2304214 2304242 29  +  .  ID=CRISPR1_REPEAT1_2304214_2304243;Name=CRISPR1_REPEAT1_2304214_2304243;Parent=CRISPR1_2304214_2305953;Note=GTGTTCCCCACGTGCGTGGGGATG
ACCESSION  CRISPRDetect  binding_site   2304243 2304274 32  +  .  ID=CRISPR1_SPACER1_2304243_2304275;Name=CRISPR1_SPACER1_2304243_2304275;Parent=CRISPR1_2304214_2305953;Note=GGATTGCTTCGCCCATCTGCCGGG
ACCESSION  CRISPRDetect  direct_repeat  2304275 2304303 29  +  .  ID=CRISPR1_REPEAT2_2304275_2304304;Name=CRISPR1_REPEAT2_2304275_2304304;Parent=CRISPR1_2304214_2305953;Note=GTGTTCCCCACGTGCGTGGGGATG
ACCESSION  CRISPRDetect  binding_site   2304304 2304335 32  +  .  ID=CRISPR1_SPACER2_2304304_2304336;Name=CRISPR1_SPACER2_2304304_2304336;Parent=CRISPR1_2304214_2305953;Note=ACCGGATGCAGTCTTAATCCCTTT
ACCESSION  CRISPRDetect  direct_repeat  2304336 2304366 30  +  .  ID=CRISPR1_REPEAT3_2304336_2304367;Name=CRISPR1_REPEAT3_2304336_2304367;Parent=CRISPR1_2304214_2305953;Note=GTGTTCCCCACGTGCGTGGGGATG
ACCESSION  CRISPRDetect  binding_site   2304367 2304398 32  +  .  ID=CRISPR1_SPACER3_2304367_2304399;Name=CRISPR1_SPACER3_2304367_2304399;Parent=CRISPR1_2304214_2305953;Note=TTATGCTGGTGCTGTCATAGATCA
ACCESSION  CRISPRDetect  direct_repeat  2304398 2304426 29  +  .  ID=CRISPR1_REPEAT4_2304398_2304427;Name=CRISPR1_REPEAT4_2304398_2304427;Parent=CRISPR1_2304214_2305953;Note=GTGTTCCCCACGTGCGTGGGGATG
ACCESSION  CRISPRDetect  binding_site   2304427 2304458 32  +  .  ID=CRISPR1_SPACER4_2304427_2304459;Name=CRISPR1_SPACER4_2304427_2304459;Parent=CRISPR1_2304214_2305953;Note=CTCTACGACGAGAAGTTTGGCCTG
ACCESSION  CRISPRDetect  direct_repeat  2304459 2304487 29  +  .  ID=CRISPR1_REPEAT5_2304459_2304488;Name=CRISPR1_REPEAT5_2304459_2304488;Parent=CRISPR1_2304214_2305953;Note=GTGTTCCCCACGTGCGTGGGGATG
ACCESSION  CRISPRDetect  binding_site   2304488 2304519 32  +  .  ID=CRISPR1_SPACER5_2304488_2304520;Name=CRISPR1_SPACER5_2304488_2304520;Parent=CRISPR1_2304214_2305953;Note=TCTATGGGAGGTGGGGAGTGAACG
ACCESSION  CRISPRDetect  direct_repeat  2304520 2304548 29  +  .  ID=CRISPR1_REPEAT6_2304520_2304549;Name=CRISPR1_REPEAT6_2304520_2304549;Parent=CRISPR1_2304214_2305953;Note=GTGTTCCCCACGTGCGTGGGGATG
ACCESSION  CRISPRDetect  binding_site   2304549 2304580 32  +  .  ID=CRISPR1_SPACER6_2304549_2304581;Name=CRISPR1_SPACER6_2304549_2304581;Parent=CRISPR1_2304214_2305953;Note=TTGAGGGCAAACGACGTTTTGCCC
ACCESSION  CRISPRDetect  direct_repeat  2304581 2304609 29  +  .  ID=CRISPR1_REPEAT7_2304581_2304610;Name=CRISPR1_REPEAT7_2304581_2304610;Parent=CRISPR1_2304214_2305953;Note=GTGTTCCCCACGTGCGTGGGGATG
ACCESSION  CRISPRDetect  binding_site   2304610 2304641 32  +  .  ID=CRISPR1_SPACER7_2304610_2304642;Name=CRISPR1_SPACER7_2304610_2304642;Parent=CRISPR1_2304214_2305953;Note=TAACGGCCCGCCCCTTCACGCGAC
ACCESSION  CRISPRDetect  direct_repeat  2304642 2304670 29  +  .  ID=CRISPR1_REPEAT8_2304642_2304671;Name=CRISPR1_REPEAT8_2304642_2304671;Parent=CRISPR1_2304214_2305953;Note=GTGTTCCCCACGTGCGTGGGGATG
ACCESSION  CRISPRDetect  binding_site   2304671 2304702 32  +  .  ID=CRISPR1_SPACER8_2304671_2304703;Name=CRISPR1_SPACER8_2304671_2304703;Parent=CRISPR1_2304214_2305953;Note=CCAAGAAAGAACGCCGAAAGGCCG
ACCESSION  CRISPRDetect  direct_repeat  2304703 2304731 29  +  .  ID=CRISPR1_REPEAT9_2304703_2304732;Name=CRISPR1_REPEAT9_2304703_2304732;Parent=CRISPR1_2304214_2305953;Note=GTGTTCCCCACGTGCGTGGGGATG
ACCESSION  CRISPRDetect  binding_site   2304732 2304763 32  +  .  ID=CRISPR1_SPACER9_2304732_2304764;Name=CRISPR1_SPACER9_2304732_2304764;Parent=CRISPR1_2304214_2305953;Note=ACGTTGAGTACGTCGGCGCCGTAC
ACCESSION  CRISPRDetect  direct_repeat  2304764 2304792 29  +  .  ID=CRISPR1_REPEAT10_2304764_2304793;Name=CRISPR1_REPEAT10_2304764_2304793;Parent=CRISPR1_2304214_2305953;Note=GTGTTCCCCACGTGCGTGGGGA
ACCESSION  CRISPRDetect  binding_site   2304793 2304824 32  +  .  ID=CRISPR1_SPACER10_2304793_2304825;Name=CRISPR1_SPACER10_2304793_2304825;Parent=CRISPR1_2304214_2305953;Note=CGGGCCTTGGCAGCGAGCAGGG
ACCESSION  CRISPRDetect  direct_repeat  2304825 2304853 29  +  .  ID=CRISPR1_REPEAT11_2304825_2304854;Name=CRISPR1_REPEAT11_2304825_2304854;Parent=CRISPR1_2304214_2305953;Note=GTGTTCCCCACGTGCGTGGGGA
ACCESSION  CRISPRDetect  binding_site   2304854 2304885 32  +  .  ID=CRISPR1_SPACER11_2304854_2304886;Name=CRISPR1_SPACER11_2304854_2304886;Parent=CRISPR1_2304214_2305953;Note=CGCACTGATGCCAGAGCCGGAG
ACCESSION  CRISPRDetect  direct_repeat  2304886 2304914 29  +  .  ID=CRISPR1_REPEAT12_2304886_2304915;Name=CRISPR1_REPEAT12_2304886_2304915;Parent=CRISPR1_2304214_2305953;Note=GTGTTCCCCACGTGCGTGGGGA
ACCESSION  CRISPRDetect  binding_site   2304915 2304946 32  +  .  ID=CRISPR1_SPACER12_2304915_2304947;Name=CRISPR1_SPACER12_2304915_2304947;Parent=CRISPR1_2304214_2305953;Note=TCGGCCATCACTGGCAAGGTGC
ACCESSION  CRISPRDetect  direct_repeat  2304947 2304975 29  +  .  ID=CRISPR1_REPEAT13_2304947_2304976;Name=CRISPR1_REPEAT13_2304947_2304976;Parent=CRISPR1_2304214_2305953;Note=GTGTTCCCCACGTGCGTGGGGA
ACCESSION  CRISPRDetect  binding_site   2304976 2305007 32  +  .  ID=CRISPR1_SPACER13_2304976_2305008;Name=CRISPR1_SPACER13_2304976_2305008;Parent=CRISPR1_2304214_2305953;Note=GCGCTTCACGGAGACGGCCTGC
ACCESSION  CRISPRDetect  direct_repeat  2305008 2305036 29  +  .  ID=CRISPR1_REPEAT14_2305008_2305037;Name=CRISPR1_REPEAT14_2305008_2305037;Parent=CRISPR1_2304214_2305953;Note=GTGTTCCCCACGTGCGTGGGGA
ACCESSION  CRISPRDetect  binding_site   2305037 2305068 32  +  .  ID=CRISPR1_SPACER14_2305037_2305069;Name=CRISPR1_SPACER14_2305037_2305069;Parent=CRISPR1_2304214_2305953;Note=TTCAGCAGGGCGTCAGGGATGG
ACCESSION  CRISPRDetect  direct_repeat  2305069 2305097 29  +  .  ID=CRISPR1_REPEAT15_2305069_2305098;Name=CRISPR1_REPEAT15_2305069_2305098;Parent=CRISPR1_2304214_2305953;Note=GTGTTCCCCACGTGCGTGGGGA
ACCESSION  CRISPRDetect  binding_site   2305098 2305129 32  +  .  ID=CRISPR1_SPACER15_2305098_2305130;Name=CRISPR1_SPACER15_2305098_2305130;Parent=CRISPR1_2304214_2305953;Note=GCTACTGTCGAAGCCGGCACCA
ACCESSION  CRISPRDetect  direct_repeat  2305130 2305158 29  +  .  ID=CRISPR1_REPEAT16_2305130_2305159;Name=CRISPR1_REPEAT16_2305130_2305159;Parent=CRISPR1_2304214_2305953;Note=GTGTTCCCCACGTGCGTGGGGA
ACCESSION  CRISPRDetect  binding_site   2305159 2305190 32  +  .  ID=CRISPR1_SPACER16_2305159_2305191;Name=CRISPR1_SPACER16_2305159_2305191;Parent=CRISPR1_2304214_2305953;Note=GCCGGATTCCGCTGCCGGGCTA
ACCESSION  CRISPRDetect  direct_repeat  2305191 2305219 29  +  .  ID=CRISPR1_REPEAT17_2305191_2305220;Name=CRISPR1_REPEAT17_2305191_2305220;Parent=CRISPR1_2304214_2305953;Note=GTGTTCCCCACGTGCGTGGGGA
ACCESSION  CRISPRDetect  binding_site   2305220 2305252 33  +  .  ID=CRISPR1_SPACER17_2305220_2305253;Name=CRISPR1_SPACER17_2305220_2305253;Parent=CRISPR1_2304214_2305953;Note=CGGGGCATGACTTCAACCCACC
ACCESSION  CRISPRDetect  direct_repeat  2305253 2305281 29  +  .  ID=CRISPR1_REPEAT18_2305253_2305282;Name=CRISPR1_REPEAT18_2305253_2305282;Parent=CRISPR1_2304214_2305953;Note=GTGTTCCCCACGTGCGTGGGGA
ACCESSION  CRISPRDetect  binding_site   2305282 2305313 32  +  .  ID=CRISPR1_SPACER18_2305282_2305314;Name=CRISPR1_SPACER18_2305282_2305314;Parent=CRISPR1_2304214_2305953;Note=TCGCACTTCCAGCCATGGCTGG
ACCESSION  CRISPRDetect  direct_repeat  2305314 2305342 29  +  .  ID=CRISPR1_REPEAT19_2305314_2305343;Name=CRISPR1_REPEAT19_2305314_2305343;Parent=CRISPR1_2304214_2305953;Note=GTGTTCCCCACGTGCGTGGGGA
ACCESSION  CRISPRDetect  binding_site   2305343 2305374 32  +  .  ID=CRISPR1_SPACER19_2305343_2305375;Name=CRISPR1_SPACER19_2305343_2305375;Parent=CRISPR1_2304214_2305953;Note=GCAGTCAAGGCTGCCGGCGGCC
ACCESSION  CRISPRDetect  direct_repeat  2305375 2305403 29  +  .  ID=CRISPR1_REPEAT20_2305375_2305404;Name=CRISPR1_REPEAT20_2305375_2305404;Parent=CRISPR1_2304214_2305953;Note=GTGTTCCCCACGTGCGTGGGGA
ACCESSION  CRISPRDetect  binding_site   2305404 2305435 32  +  .  ID=CRISPR1_SPACER20_2305404_2305436;Name=CRISPR1_SPACER20_2305404_2305436;Parent=CRISPR1_2304214_2305953;Note=GCCAGCAGGGATGCCAGCACGC
ACCESSION  CRISPRDetect  direct_repeat  2305436 2305464 29  +  .  ID=CRISPR1_REPEAT21_2305436_2305465;Name=CRISPR1_REPEAT21_2305436_2305465;Parent=CRISPR1_2304214_2305953;Note=GTGTTCCCCACGTGCGTGGGGA
ACCESSION  CRISPRDetect  binding_site   2305465 2305496 32  +  .  ID=CRISPR1_SPACER21_2305465_2305497;Name=CRISPR1_SPACER21_2305465_2305497;Parent=CRISPR1_2304214_2305953;Note=CAGTGACGGCAGCAGACGCGGC
ACCESSION  CRISPRDetect  direct_repeat  2305497 2305525 29  +  .  ID=CRISPR1_REPEAT22_2305497_2305526;Name=CRISPR1_REPEAT22_2305497_2305526;Parent=CRISPR1_2304214_2305953;Note=GTGTTCCCCACGTGCGTGGGGA
ACCESSION  CRISPRDetect  binding_site   2305526 2305557 32  +  .  ID=CRISPR1_SPACER22_2305526_2305558;Name=CRISPR1_SPACER22_2305526_2305558;Parent=CRISPR1_2304214_2305953;Note=TCGGTAGACGCACAGATGGTCG
ACCESSION  CRISPRDetect  direct_repeat  2305558 2305586 29  +  .  ID=CRISPR1_REPEAT23_2305558_2305587;Name=CRISPR1_REPEAT23_2305558_2305587;Parent=CRISPR1_2304214_2305953;Note=GTGTTCCCCACGTGCGTGGGGA
ACCESSION  CRISPRDetect  binding_site   2305587 2305618 32  +  .  ID=CRISPR1_SPACER23_2305587_2305619;Name=CRISPR1_SPACER23_2305587_2305619;Parent=CRISPR1_2304214_2305953;Note=GCGCAGGGCAAAGCCAAGGTCA
ACCESSION  CRISPRDetect  direct_repeat  2305619 2305647 29  +  .  ID=CRISPR1_REPEAT24_2305619_2305648;Name=CRISPR1_REPEAT24_2305619_2305648;Parent=CRISPR1_2304214_2305953;Note=GTGTTCCCCACATGCGTGGGGA
```

CRISPRCasFinder

- **.json** -> visualization in CRISPRCasViewer


```
{
"Date":"25/10/2019_8:9:22",
"Version":"4.2.17",
"Command":"perl CRISPRCasFinder.pl -levelMin 3 -cas -in /home/Pseudomonas_aeruginosa/PaL
"Sequences":
[{
"Id":"1",
"Description":"Unknown",
"AT":33.7792277109783,
"Length":6596779,
"Summary_CRISPR-Cas":"",
"Crisprs":[
{
"Name": "1_1",
"Start": 2293915,
"End": 2294980,
"DR_Consensus": "GTGTTCCCCACGGGTGTGGGGATGAACCG",
"Repeat_ID": "Unknown",
"DR_Length": 29,
"Spacers": 17,
"Potential_Orientation": "+",
"CRISPRDirection": "ND",
"Evidence_Level": 4,
"Conservation_DRs": 95.7304354599955,
"Conservation_Spacers": 0,
"Regions": [
{
"Type": "LeftFLANK",
"Start": 2293815,
"End": 2293914,
"Sequence": "TGAGTACGGCCCTCATTTCCAGGAGCGGCGCGAGGGCCGCTTGGCCCGGTGGAATTTTGCTGTTGTTTTTCTTTT
"Leader": 1,
"AT": 49
```

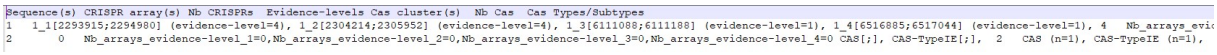

- TSV folder: **.tsv+.xls** for:
  - **Cas_REPORT**

```
##############################################
1 ( Unknown )
----------------------------------------------
### System: CAS-TypeIE (UserReplicon_CAS-TypeIE_1)
#SequenceID Cas-type/subtype    Gene status System  Type    Begin   End Strand  Other_information
PaLo1_02144 Cas3_0_I    accessory   CAS
PaLo1_02145 Cse1_0_IE   mandatory   CAS-TypeIE
PaLo1_02146 Cse2_0_IE   mandatory   CAS-TypeIE
PaLo1_02147 Cas7_0_IE   mandatory   CAS-TypeIE
PaLo1_02148 Cas5_0_IE   mandatory   CAS-TypeIE
PaLo1_02149 Cas6_0_IE   mandatory   CAS-TypeIE
PaLo1_02150 Cas1_0_IE   mandatory   CAS-TypeIE
PaLo1_02151 Cas2_0_IE   mandatory   CAS-TypeIE
####Summary system CAS-TypeIE:begin=;end=:{sequenceID=1} : [Cas3_0_I (,,); Cse1_0_IE (,,); Cse2_0_IE


##############################################
2 ( Unknown )
----------------------------------------------
### System: CAS (CAS_putative)
#SequenceID Cas-type/subtype    Gene status System  Type    Begin   End Strand  Other_information
PaLo1_00479 Cas3_0_I    accessory   CAS
PaLo1_01544 Cas3_0_I    accessory   CAS
PaLo1_01750 Cas3_0_I    accessory   CAS
PaLo1_02144 Cas3_0_I    accessory   CAS
PaLo1_03983 Cas3_0_I    accessory   CAS
PaLo1_04151 Cas3_0_I    accessory   CAS
PaLo1_04355 Cas3_1_I    accessory   CAS
####Summary system CAS:begin=;end=:{sequenceID=2} : [Cas3_0_I (,,); Cas3_0_I (,,); Cas3_0_I (,,); Cas
```

  - **Crisprs_REPORT**

Strain	Sequence	Sequence_basename	Duplicated_Spacers	CRISPR_Id	CRISPR_Start	CRISPR_End	CRISPR_Length	Potential_Orientation	(AT%)	CRISPRDirection	Consensus_Repeat	Repeat_ID (CRISPRdb)	Nb
Unknown 1	1	0	1_1	2293915	2294980	1065	Forward	Unknown	GTGTTCCCCACGGGTGTGGGGATGAACCG	Unknown	0	29	17	32	0	16	0.888888888888889	86.2068965517241	95.7304354599955	0	0	61	0.90625
Unknown 1	1	0	1_2	2304214	2305952	1738	Forward	Unknown	GTGTTCCCCACGTGCGTGGGGATGAACCG	Unknown	0	29	28	32.0714285714286	0.262265264156481	22	0.758620689655172	89.6551724137931	95.9713

- **CRISPR-Cas_summary** (CRISPRs and Cas per sequence)



```
Sequence(s) CRISPR array(s) Nb CRISPRs  Evidence-levels Cas cluster(s)  Nb Cas  Cas Types/Subtypes
1   1_1[2293915;2294980] (evidence-level=4), 1_2[2304214;2305952] (evidence-level=4), 1_3[6111088;6111188] (evidence-level=1), 1_4[6516885;6517044] (evidence-level=1), 4   Nb_arrays_evi
2       0   Nb_arrays_evidence-level_1=0,Nb_arrays_evidence-level_2=0,Nb_arrays_evidence-level_3=0,Nb_arrays_evidence-level_4=0 CAS[;], CAS-TypeIE[;],  2   CAS (n=1), CAS-TypeIE (n=1),
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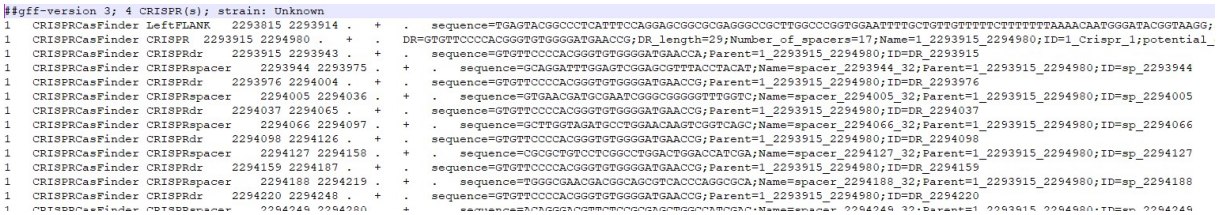
- GFF folder: **.gff** and **annotation.gff** per sequence in input file



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##gff-version 3; 4 CRISPR(s); strain: Unknown
1   CRISPRCasFinder LeftFLANK   2293815 2293914 .   +   .   sequence=TGAGTACGGCCCTCATTTCCAGGAGCGGCGCGAGGGCCGCTTGGCCCGGTGGAATTTTGCTGTTGTTTTTCTTTTTTTAAAACAATGGGATACGGTAAGG;
1   CRISPRCasFinder CRISPR  2293915 2294980 .   +   .   DR=GTGTTCCCCACGGGTGTGGGGATGAACCG;DR_length=29;Number_of_spacers=17;Name=1_2293915_2294980;ID=1_Crispr_1;potential_
1   CRISPRCasFinder CRISPRdr    2293915 2293943 .   +   .   sequence=GTGTTCCCCACGGGTGTGGGGATGAACCA;Parent=1_2293915_2294980;ID=DR_2293915
1   CRISPRCasFinder CRISPRspacer    2293944 2293975 .   +   .   sequence=GCAGGATTTGGAGTCGGAGCGTTTACCTACAT;Name=spacer_2293944_32;Parent=1_2293915_2294980;ID=sp_2293944
1   CRISPRCasFinder CRISPRdr    2293976 2294004 .   +   .   sequence=GTGTTCCCCACGGGTGTGGGGATGAACCG;Parent=1_2293915_2294980;ID=DR_2293976
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1   CRISPRCasFinder CRISPRdr    2294159 2294187 .   +   .   sequence=GTGTTCCCCACGGGTGTGGGGATGAACCG;Parent=1_2293915_2294980;ID=DR_2294159
1   CRISPRCasFinder CRISPRspacer    2294188 2294219 .   +   .   sequence=TGGGCGAACGACGGCAGCGTCACCCAGGCGCA;Name=spacer_2294188_32;Parent=1_2293915_2294980;ID=sp_2294188
1   CRISPRCasFinder CRISPRdr    2294220 2294248 .   +   .   sequence=GTGTTCCCCACGGGTGTGGGGATGAACCG;Parent=1_2293915_2294980;ID=DR_2294220
1   CRISPRCasFinder CRISPRspacer    2294249 2294280 .   +   .   sequence=ACAGGGACGTTTCTCCCCGAGCGTTGGCCATTCCGAC;Name=spacer_2294249_32;Parent=1_2293915_2294980;ID=sp_2294249
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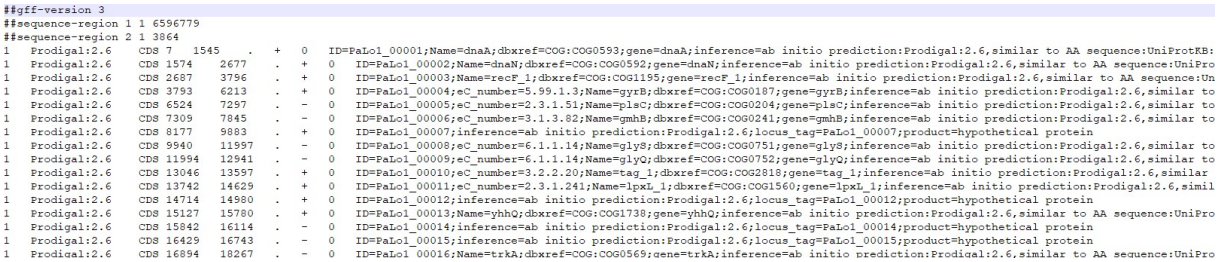

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##sequence-region 1 1 6596779
##sequence-region 2 1 3864
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1   Prodigal:2.6    CDS 1574    2677    .   +   0   ID=PaLo1_00002;Name=dnaN;dbxref=COG:COG0592;gene=dnaN;inference=ab initio prediction:Prodigal:2.6,similar to AA sequence:UniPro
1   Prodigal:2.6    CDS 2687    3796    .   +   0   ID=PaLo1_00003;Name=recF_1;dbxref=COG:COG1195;gene=recF_1;inference=ab initio prediction:Prodigal:2.6,similar to AA sequence:Un
1   Prodigal:2.6    CDS 3793    6213    .   +   0   ID=PaLo1_00004;eC_number=5.99.1.3;Name=gyrB;dbxref=COG:COG0187;gene=gyrB;inference=ab initio prediction:Prodigal:2.6,similar to
1   Prodigal:2.6    CDS 6524    7297    .   -   0   ID=PaLo1_00005;eC_number=2.3.1.51;Name=plsC;dbxref=COG:COG0204;gene=plsC;inference=ab initio prediction:Prodigal:2.6,similar to
1   Prodigal:2.6    CDS 7309    7845    .   -   0   ID=PaLo1_00006;eC_number=3.1.3.82;Name=gmhB;dbxref=COG:COG0241;gene=gmhB;inference=ab initio prediction:Prodigal:2.6,similar to
1   Prodigal:2.6    CDS 8177    9883    .   +   0   ID=PaLo1_00007;inference=ab initio prediction:Prodigal:2.6;locus_tag=PaLo1_00007;product=hypothetical protein
1   Prodigal:2.6    CDS 9940    11997   .   -   0   ID=PaLo1_00008;eC_number=6.1.1.14;Name=glyS;dbxref=COG:COG0751;gene=glyS;inference=ab initio prediction:Prodigal:2.6,similar to
1   Prodigal:2.6    CDS 11994   12941   .   -   0   ID=PaLo1_00009;eC_number=6.1.1.14;Name=glyQ;dbxref=COG:COG0752;gene=glyQ;inference=ab initio prediction:Prodigal:2.6,similar to
1   Prodigal:2.6    CDS 13046   13597   .   +   0   ID=PaLo1_00010;eC_number=3.2.2.20;Name=tag_1;dbxref=COG:COG2818;gene=tag_1;inference=ab initio prediction:Prodigal:2.6,similar
1   Prodigal:2.6    CDS 13742   14629   .   +   0   ID=PaLo1_00011;eC_number=2.3.1.241;Name=lpxL_1;dbxref=COG:COG1560;gene=lpxL_1;inference=ab initio prediction:Prodigal:2.6,simil
1   Prodigal:2.6    CDS 14714   14980   .   +   0   ID=PaLo1_00012;inference=ab initio prediction:Prodigal:2.6;locus_tag=PaLo1_00012;product=hypothetical protein
1   Prodigal:2.6    CDS 15127   15780   .   +   0   ID=PaLo1_00013;Name=yhhQ;dbxref=COG:COG1738;gene=yhhQ;inference=ab initio prediction:Prodigal:2.6,similar to AA sequence:UniPro
1   Prodigal:2.6    CDS 15842   16114   .   -   0   ID=PaLo1_00014;inference=ab initio prediction:Prodigal:2.6;locus_tag=PaLo1_00014;product=hypothetical protein
1   Prodigal:2.6    CDS 16429   16743   .   -   0   ID=PaLo1_00015;inference=ab initio prediction:Prodigal:2.6;locus_tag=PaLo1_00015;product=hypothetical protein
1   Prodigal:2.6    CDS 16894   18267   .   -   0   ID=PaLo1_00016;Name=trkA;dbxref=COG:COG0569;gene=trkA;inference=ab initio prediction:Prodigal:2.6,similar to AA sequence:UniPro
```
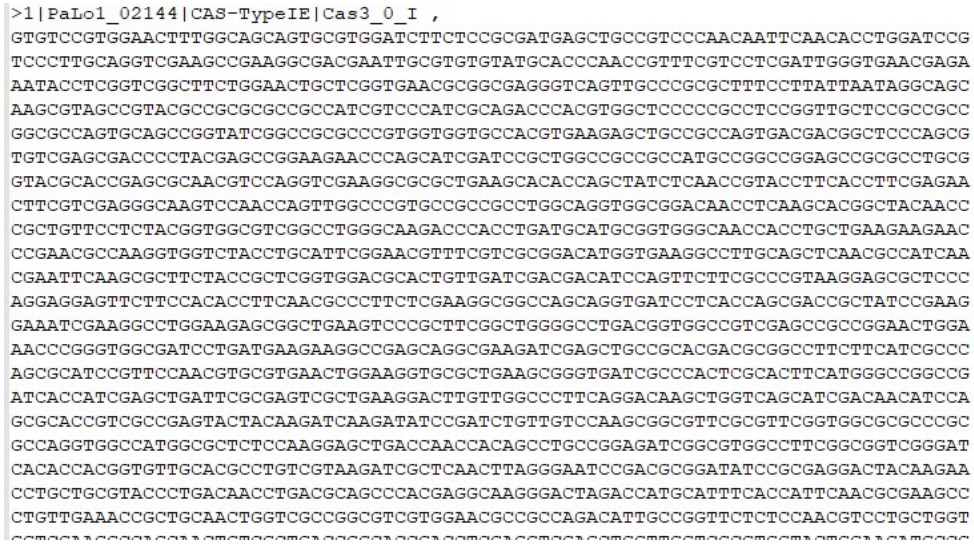

- **rawCas.fna** (not existing if no Cas found)



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- **CRISPRs.fna**

```
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>1_2 2304214,2305952
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```

More possible using command-line options (clustering etc.)